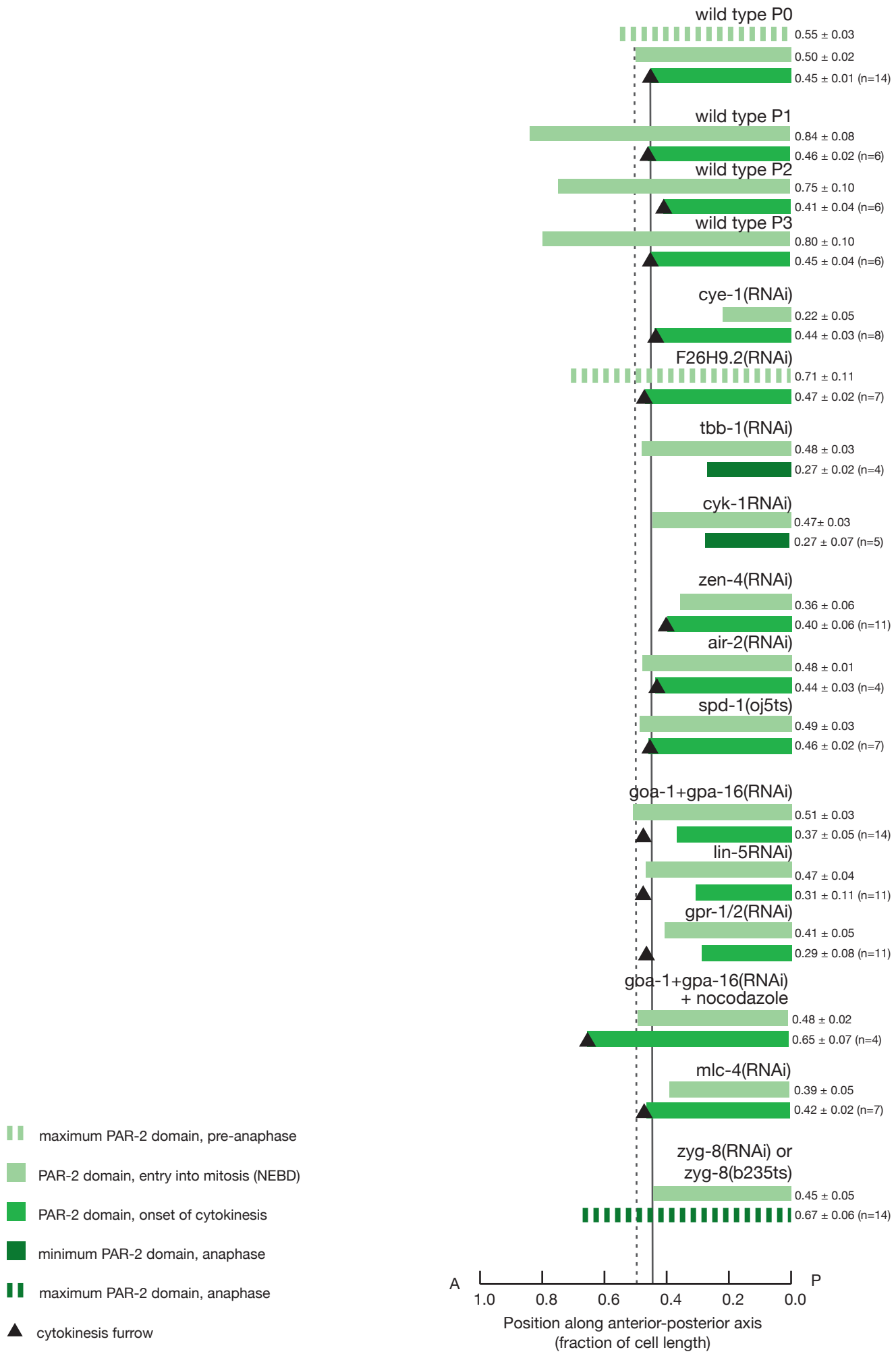
wild type P0
0.55 ± 0.03
0.50 ± 0.02
0.45 ± 0.01 (n=14)
wild type P1
0.84 ± 0.08
0.46 ± 0.02 (n=6)
wild type P2
0.75 ± 0.10
0.41 ± 0.04 (n=6)
wild type P3
0.80 ± 0.10
0.45 ± 0.04 (n=6)
cye-1(RNAi)
0.22 ± 0.05
0.44 ± 0.03 (n=8)
F26H9.2(RNAi)
0.71 ± 0.11
0.47 ± 0.02 (n=7)
tbb-1(RNAi)
0.48 ± 0.03
0.27 ± 0.02 (n=4)
cyk-1RNAi)
0.47± 0.03
0.27 ± 0.07 (n=5)
zen-4(RNAi)
0.36 ± 0.06
0.40 ± 0.06 (n=11)
air-2(RNAi)
0.48 ± 0.01
0.44 ± 0.03 (n=4)
spd-1(oj5ts)
0.49 ± 0.03
0.46 ± 0.02 (n=7)
goa-1+gpa-16(RNAi)
0.51 ± 0.03
0.37 ± 0.05 (n=14)
lin-5RNAi)
0.47 ± 0.04
0.31 ± 0.11 (n=11)
gpr-1/2(RNAi)
0.41 ± 0.05
0.29 ± 0.08 (n=11)
gba-1+gpa-16(RNAi)
+ nocodazole
0.48 ± 0.02
0.65 ± 0.07 (n=4)
mlc-4(RNAi)
0.39 ± 0.05
0.42 ± 0.02 (n=7)
zyg-8(RNAi) or
zyg-8(b235ts)
0.45 ± 0.05
0.67 ± 0.06 (n=14)
A
P
1.0
0.8
0.6
0.4
0.2
0.0
Position along anterior-posterior axis
(fraction of cell length)
maximum PAR-2 domain, pre-anaphase
PAR-2 domain, entry into mitosis (NEBD)
PAR-2 domain, onset of cytokinesis
minimum PAR-2 domain, anaphase
maximum PAR-2 domain, anaphase
cytokinesis furrow